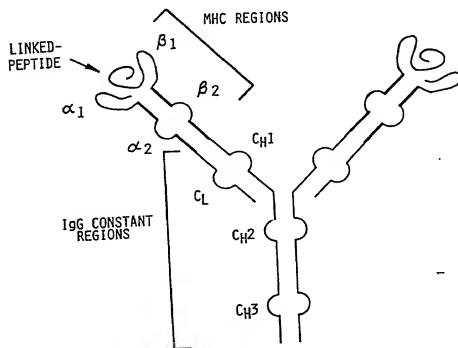
**FIG. 1B****FIG. 1C**

TOTAL RNA ISOLATED  
FROM A20 CELLS

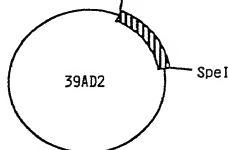
SYNTHESIS OF FIRST STRAND cDNA USING  
OPR101 OLIGONUCLEOTIDE PRIMER

I-A d  $\alpha$ CHAIN  
SPECIFIC cDNA

PCR AMPLIFICATION WITH  
OPR101 & OPR100 PRIMERS

NcoI SpeI  
 $\alpha$ 1- $\alpha$ 2 PCR  
PRODUCT

NcoI/SpeI  
DIGEST

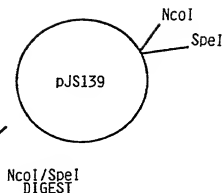
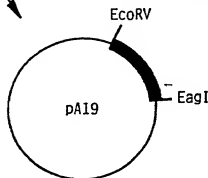


TEMPLATE FOR PCR  
AMPLIFICATIONS

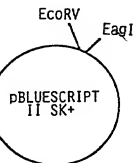
PCR WITH OPR107  
& OPR108 PRIMERS

EcoRV EagI  
 $\alpha$ 1- $\alpha$ 2 PCR  
PRODUCT

EcoRV/EagI  
DIGEST



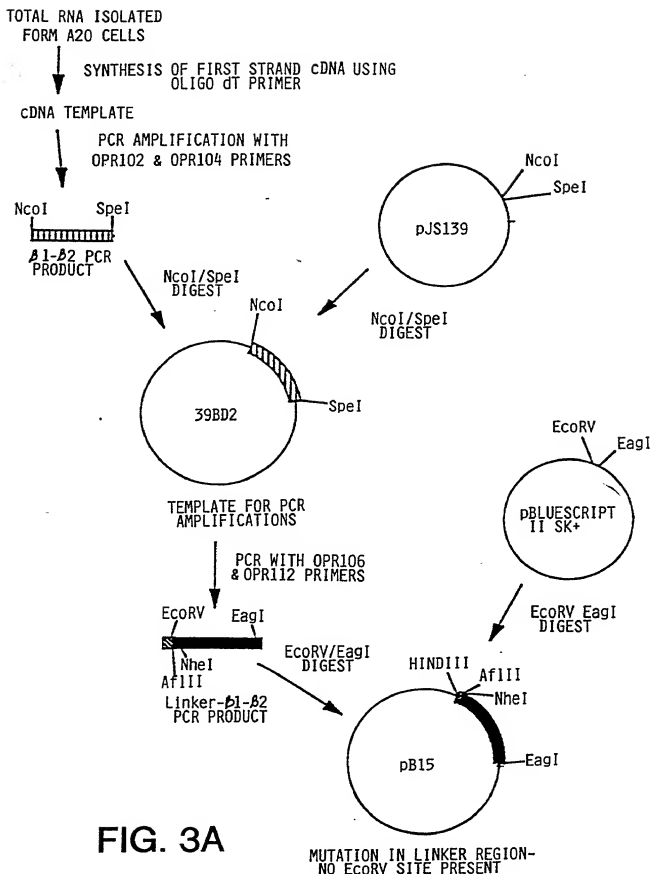
NcoI/SpeI  
DIGEST



EcoRV/EagI DIGEST

FIG. 2

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10E050-49184860



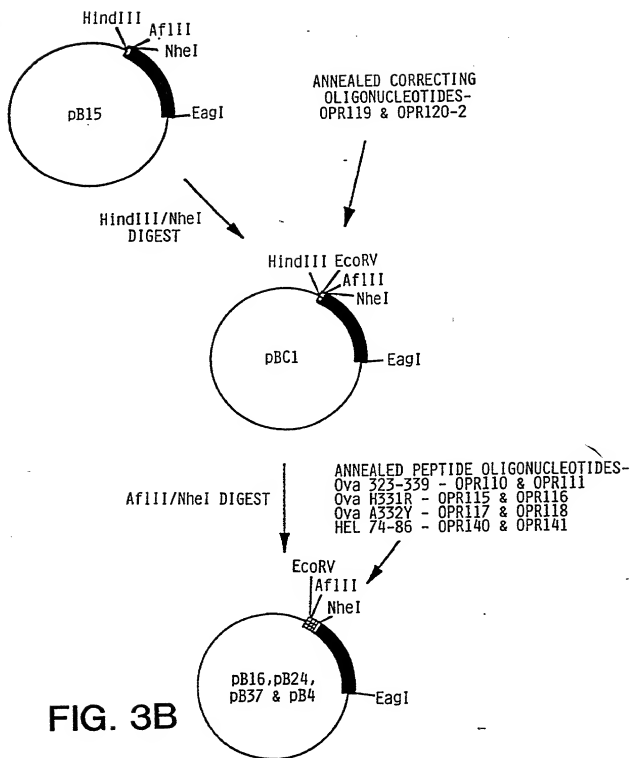


FIG. 3B

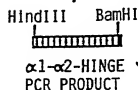
00848164-050301

TOTAL RNA ISOLATED  
FROM BLCL K68 CELLS

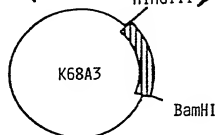
↓  
SYNTHESIS OF FIRST STRAND cDNA USING  
OLIGO-dT PRIMER

↓  
cDNA  
TEMPLATE

PCR AMPLIFICATION WITH  
DRIA-B & DRIA-F PRIMERS

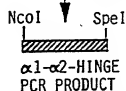


HindIII/BamHI  
DIGEST

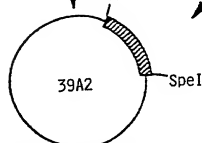


TEMPLATE FOR PCR  
AMPLIFICATIONS

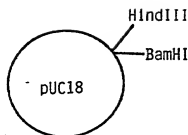
PCR WITH AF-N &  
AB-S PRIMERS



NcoI/SpeI DIGEST



TEMPLATE FOR PCR  
AMPLIFICATIONS



HindIII/BamHI  
DIGEST

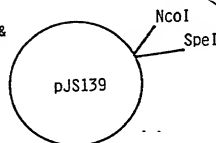
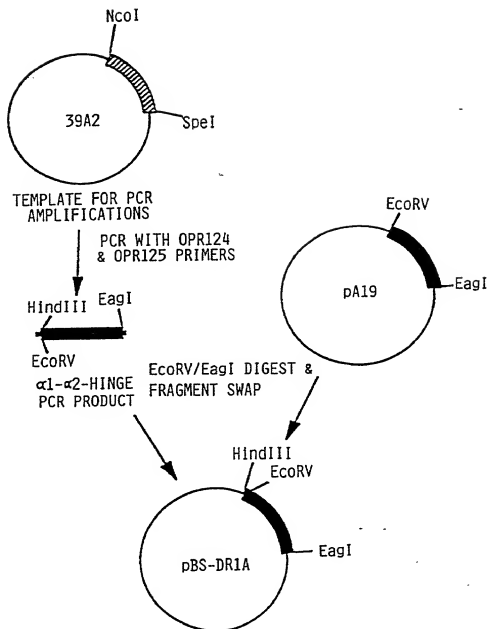


FIG. 4A

0948164-050301

**FIG. 4B**

TOTAL RNA ISOLATED  
FROM BLCL K68 CELLS

SYNTHESIS OF FIRST STRAND cDNA USING  
OLIGO-dT PRIMER

cDNA  
TEMPLATE

PCR AMPLIFICATION WITH  
DR1B-B & DR1B-F PRIMERS

HindIII BamHI  
β1-β2-HINGE PCR  
PRODUCT

HindIII/BamHI  
DIGEST

HindIII/BamHI  
DIGEST

HindIII

BamHI

pB712

JS143,3

TEMPLATE FOR PCR  
AMPLIFICATIONS

PCR WITH BF-NN  
& BB-S PRIMERS

NcoI SpeI

β1-β2-HINGE  
PCR PRODUCT

FIG. 5A

0948164-050301

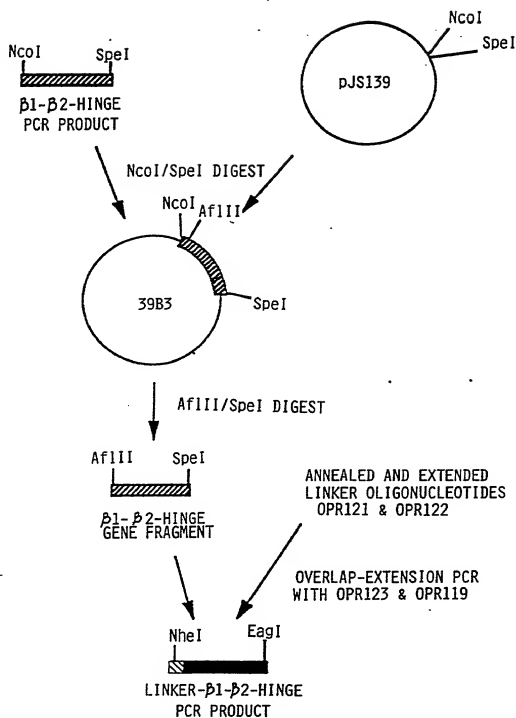


FIG. 5B



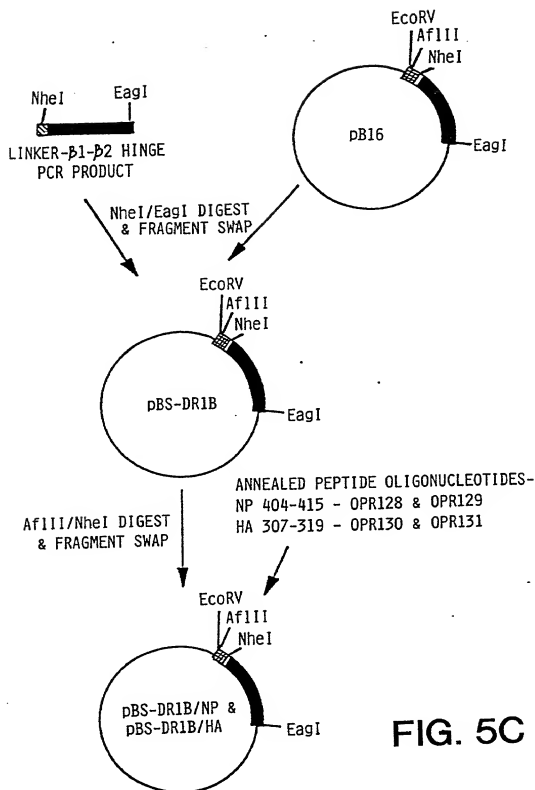


FIG. 5C

TOTAL RNA ISOLATED FROM  
SJL MOUSE SPLEEN CELLS

↓  
SYNTHESIS OF FIRST STRAND cDNA USING  
OPR101 OLIGONUCLEOTIDE PRIMER

I-A S  $\alpha$ CHAIN  
SPECIFIC cDNA

↓  
PCR AMPLIFICATION WITH  
OPR100 & OPR101 PRIMERS

NcoI SpeI  
α1-α2PCR  
PRODUCT

↓  
PCR AMPLIFICATION WITH  
OPR107 & OPR108 PRIMERS

EcoRV EagI  
α1-α2 PCR  
PRODUCT

↓  
EcoRV/EagI DIGEST  
& FRAGMENT SWAP

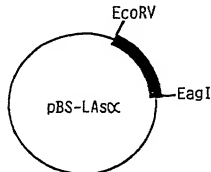
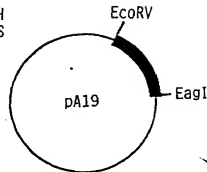


FIG. 6

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TOTAL RNA ISOLATED FROM  
SJL MOUSE SPLEEN CELLS

↓  
SYNTHESIS OF FIRST STRAND cDNA USING  
OPR106 PRIMER

I-A<sup>S</sup>  $\beta$  SPECIFIC  
cDNA TEMPLATE

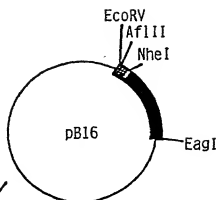
↓  
PCR AMPLIFICATION WITH  
VW310 & OPR106 PRIMERS

$\beta$ 1- $\beta$ 2 PCR PRODUCT

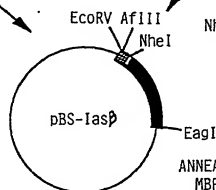
↓  
PCR AMPLIFICATION WITH  
VW309 & OPR106 PRIMERS

NheI EagI  
LINKER- $\beta$ 1- $\beta$ 2  
PCR PRODUCT

NheI/EagI DIGEST &  
FRAGMENT SWAP



NheI/EagI  
DIGEST



ANNEALED PEPTIDE OLIGONUCLEOTIDES-  
MBP 91-103 - VW315 & VW316  
PLP 139-151 - VW313 & VW314  
MBP 1-14 - VW317 & VW318

AflIII/NheI DIGEST  
& FRAGMENT SWAP

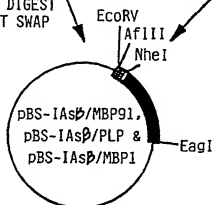


FIG. 7

09849164-050301

I-Ad/I-As PCR PRIMERS AND CLONING OLIGONUCLEOTIDES 12 / 69  
(RESTRICTION SITE ARE UNDERLINED).

OPR100  
5'-GGG GGG GCC ATG GCC GAA GAC GAC GAC ATT GAG GCC GAC-3'

OPR101  
5'-GGG GCG ACT AGT CCA GTG TTT CAG AAC CGG CTC-3'

OPR107  
5'-CCC CCC GAT ATC TCA GCT TCC AGC AGT GGA GAC GAC ATT GAG  
GCC G-3'

OPR108  
5'-CCC CCC CGG CCG CTA CTT ACG TTT CCA GTG TTT CAG AAC CGG  
C-3'

OPR102  
5'-GGG GGG GCC ATG GCC GGA AAC TCC GAA AGG CAT TTC G-3'

OPR104  
5'-GGG GCG ACT AGT CCA CTC CAC AGT GAT GGG GC-3'

OPR106  
5'-CCC CCC CGG CCG TAC CTG AGG ACC ACT CCA CAG TGA TGG-3'

OPR112  
5'-CCC CCC GAT ATC ACA GGT GTC TTA AGT GCT AGC GGA GGG GGC  
GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC-3'

OPR119  
5'-AGC TTG ATA TCA CAG GTG TCT TAA GTG GAG-3'.

OPR120-2  
5'-CTA GCT CCA CTT AAG ACA CCT GTG ATA TCA-3'

VW310  
5'-TCC GGA GGC GGC GGA GAC TCC GAA AGG CAT TTC G-3'

VW309  
5'-CGA TCG CTA GCG GCG GTG GTG GTT CCG GTG GCG GCG GAG-3'

OPR136  
5'-CCC CCC AGG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC  
TG-3'

OPR139  
5'-CCC CCC GAG CTC GAA TTC TCA TAA AGG CCC TGG GTG TCT G-3'

OPR132  
5'-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA  
GC-3'

OPR133  
5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134  
5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135  
5'-CCC CCC GAG CTC GAA TTC TCA CTG CAG GAG CCC TGC TGG-3'

FIG. 8A

## HLA-DRI PCR PRIMERS AND CLONING OLIGONUCLEOTIDES.

DRIA-F  
5'-GGG GGG AAG CTT ATG ATC AAA GAA GAA CAT GTG ATC ATC-3'

DRIA-B  
5'-GCG GCG GGA TCC GTT CTC TGT AGT CTC TGG GAG AGG-3'

DRIB-F  
5'-GGG GGG AAG CTT ATG GGG GAC ACC CGA CCA CGT TTC TTG TGG  
CAG C-3'

AF-N  
5'-GGG GGG GCC ATG GCC ATC AAA GAA GAA CAT GTG ATC ATC-3'

AB-S  
5'-GCG GCG ACT AGT GTT CTC TGT AGT CTC TGG GAG AGG-3'

OPRI24  
5'-GGG GGG AAG CTT GAT ATC TCA GCT TCC AGC AGT AGT ATC AAA  
GAA GAA CAT GTG ATC-3'

OPRI25  
5'-GGG GGG CGG CCG CTA CTT ACG TTT CTC TGG GAG AGG GCT TGG  
AGC-3'

DRIB-B  
5'-GCG GCG GGA TCC CTT GCT CTG TGC AGA TTC AGA CC-3'

BF-NN  
5'-GGG GGG GCC ATG GCC GGA TCC GCT AGC GGG GAC ACC CGA CCA  
CGT TTC TTG-3'

BB-S  
5'-GCG GCG ACT AGT CTT GCT CTG TGC AGA TTC AGA CCG-3'

OPRI21  
5'-GTT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGG TCC GGA GGT  
GGT GGG GAC ACC CG-3'

OPRI22  
5'-GAA ATG ACA TTC AAA CTT CAG CTG CCA CAA GAA ACG TGG TCG  
GGT GTC CCC ACC ACC-3'

OPRI23  
5'-GGG GGG CGG CCG TAC CTG AGG ACT TGC TCT GTG CAG ATT CAG-  
3'

FIG. 8B

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## PEPTIDE OLIGONUCLEOTIDES.

Ova 323-339

OPR110

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC GCT GAA ATC  
AAC GAA GCT GGT CGT G-3'

OPR111

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC TGA GCA GCG TGA  
ACA GCC TGA GAG ATA C-3'

Ova H331R

OPR115

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CGG GCT GAA ATC  
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC CGA GCA GCG TGA  
ACA GCC TGA GAG ATA C-3'

Ova A332Y

OPR117

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC TAC GAA ATC  
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA TAG TGA GCA GCG TGA  
ACA GCC TGA GAG ATA C-3'

HEL 74-86

OPR140

5'-TTA AGT AAC CTG TGC AAC ATC CCC TGC AGC GCC CTG CTG AGC  
TCC G-3'

OPR141

5'-CTA GCG GAG CTC AGC AGG GCG CTG CAG GGG ATG TTG CAC AGG  
TTA C-3'

NP 404-415

OPR128

5'-TTA AGT CAG ATC AGC GTG CAG CCC GCC TTC AGC GTG CAG G-3'

FIG. 8C

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OPR129  
5'-CTA GGC TGC ACG CTG AAG GCG GGC TGA ACG CTG ATC TGA C-3'

HA 307-319

OPR130  
5'-TTA AGT CCC AAG TAC GTG AAG CAG AAC ACC CTG AAG CTG GCC  
ACC G-3'

OPR131

5'-CTA GCG GTG GCC AGC TTC AGG GTG TTC TGC TTC ACG TAC TTG  
GGA C-3'

MBP 91-103

VW315  
5'-TTA AGT CAC TAT GGC TCC CTG CCG CAG AAG TCC CAG CAC GGG  
CGC G-3'

VW316

5'-CTA GCG CGC CCG TGC TGG GAC TTC TGC GGC AGG GAG CCA TAG  
TGA C-3'

PLP 139-151

VW313  
5'-TTA CAT CAC TCC CTG GGC AAG TGG CTG GGC CAC CCG GAC AAG  
TTC G-3'

VW314

5'-CTA GCG AAC TTG TTC GGG TGG CCC AGC CAC TTG CCC AGG GAG  
TGA C-3'

MBP 1-14

VW317  
5'-TTA AGT ATG GCA TCC CAG AAG CGC CCG TCC CAG CGC TCC AAG  
TAC CTG G-3'

VW316

5'-CTA GCC AGG TAC TTG GAG CGC TGG GAC GGG CGC TTC TGG GAT  
GCC ATA C-3'

**FIG. 8D**







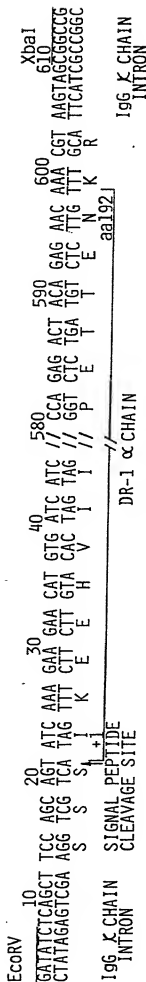


FIG. 9E

RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST



FIG. 9F

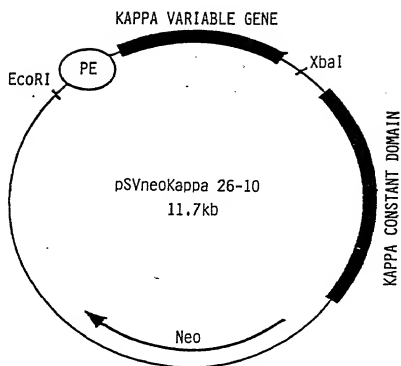


FIG. 10A

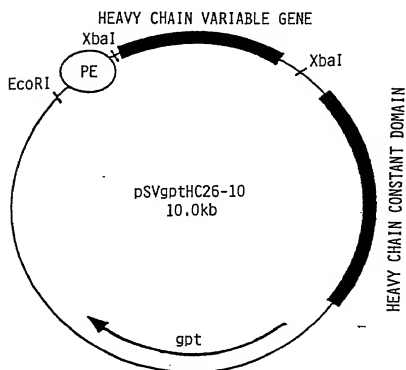


FIG. 10B

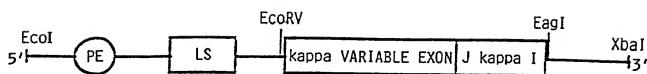


FIG. 11A

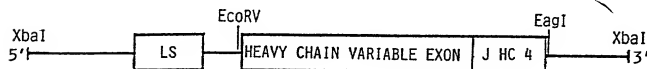


FIG. 11B

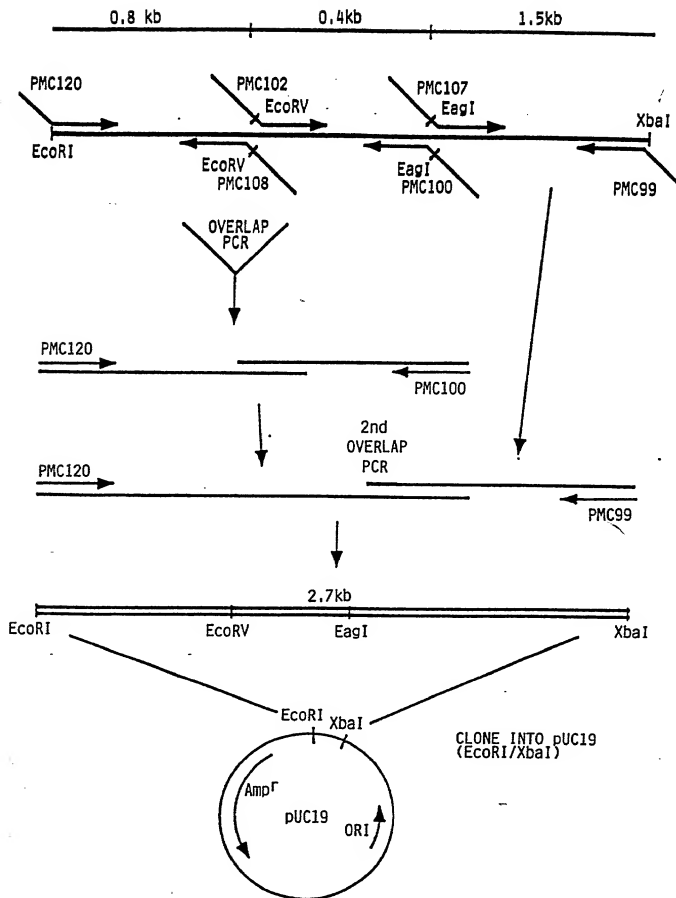


FIG. 12

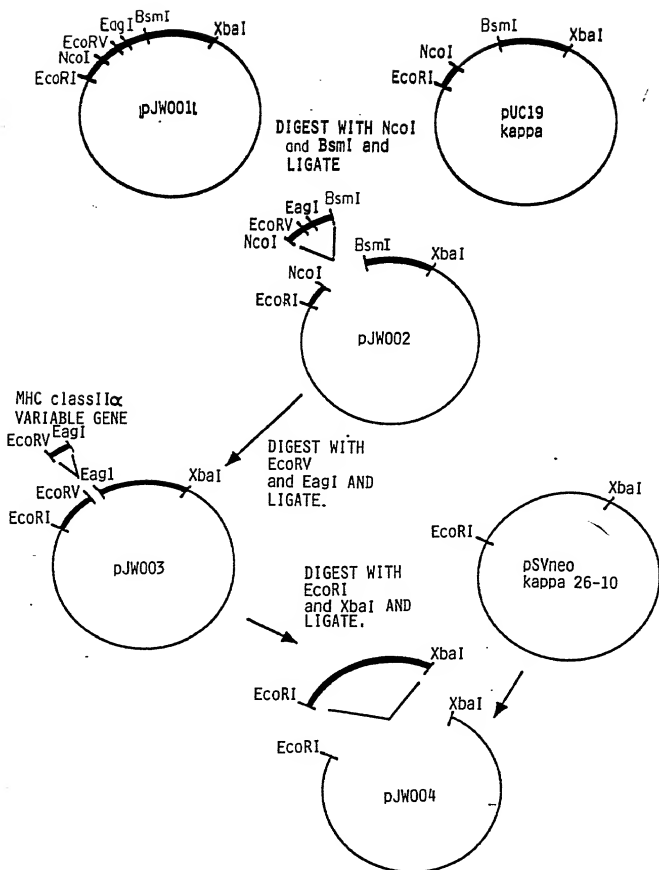


FIG. 13

PRIMER LIST

PMC-33

PMC-77

PMC-111

PMC-114

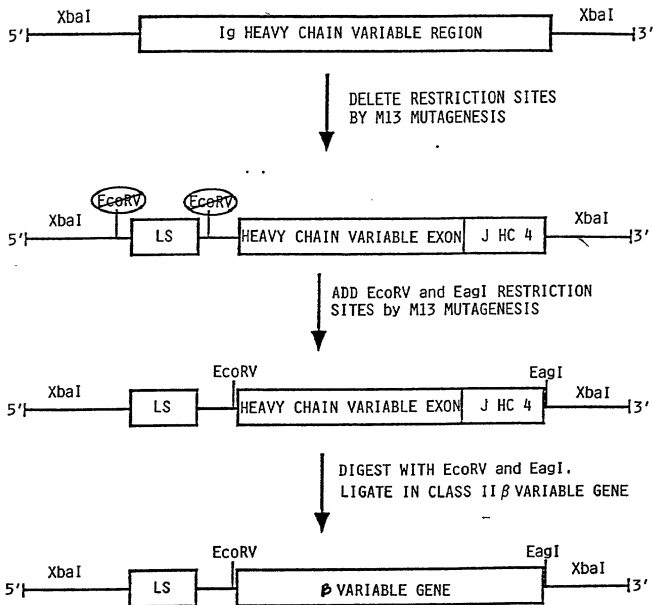
SEQUENCE

[5'GCTCAGCTGTCTTGTTCAGTACTGATC3']

[5'GTAAGTAGCGGCCG3']

[5'GGTATGTAAAAATAACATCACAG3']

[5'GCTTTGCTTACGGAGTTACTC3']

**FIG. 14****FIG. 15**

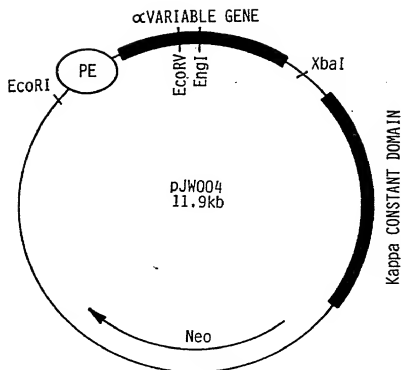


FIG. 16A

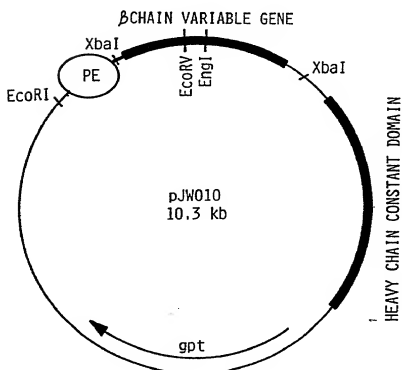


FIG. 16B



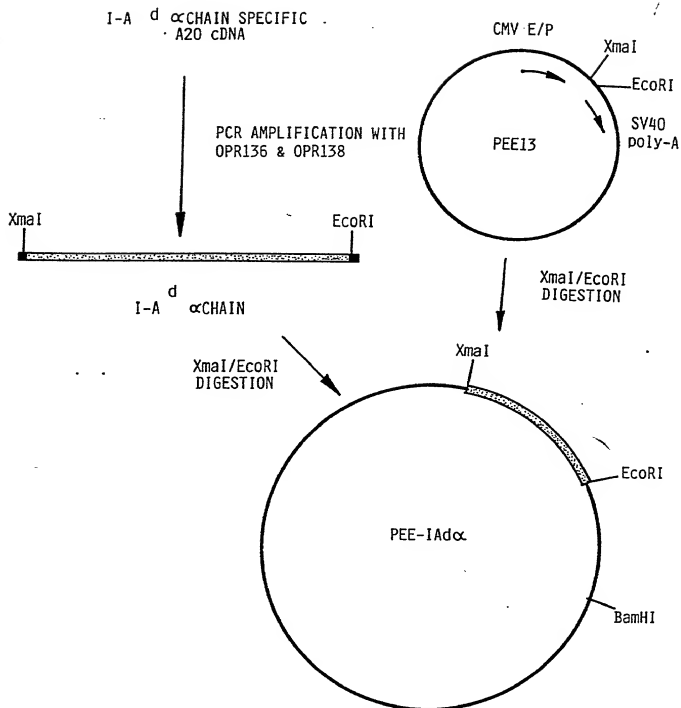


FIG. 17A

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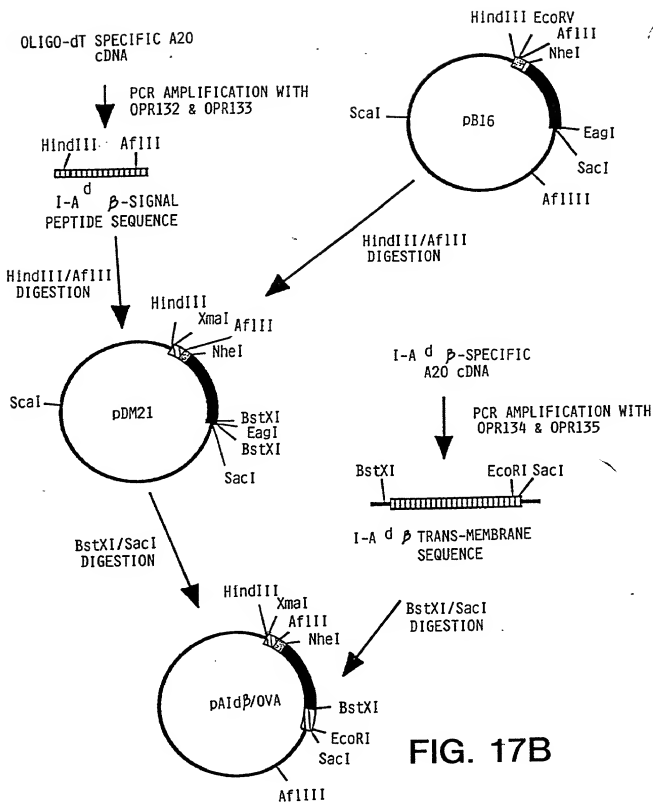


FIG. 17B

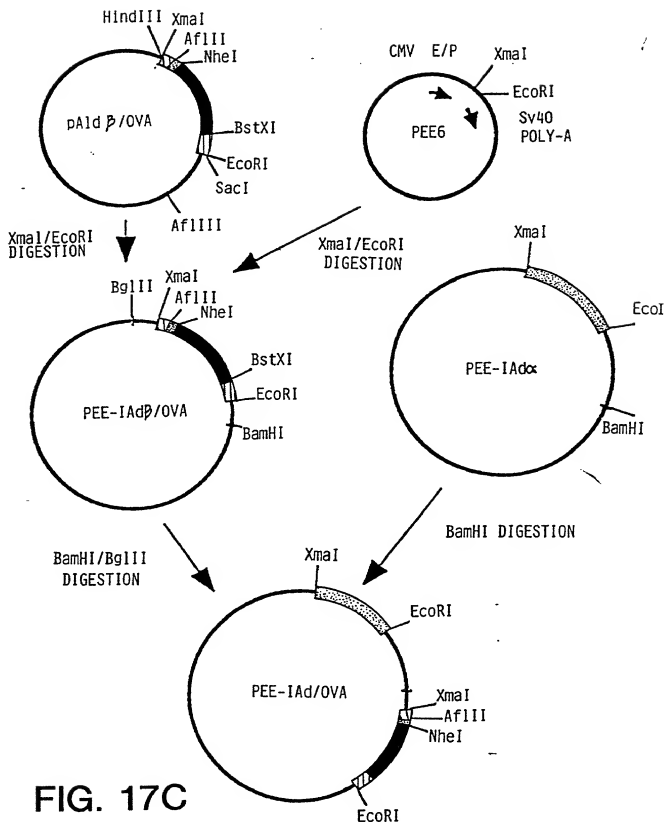


FIG. 17C

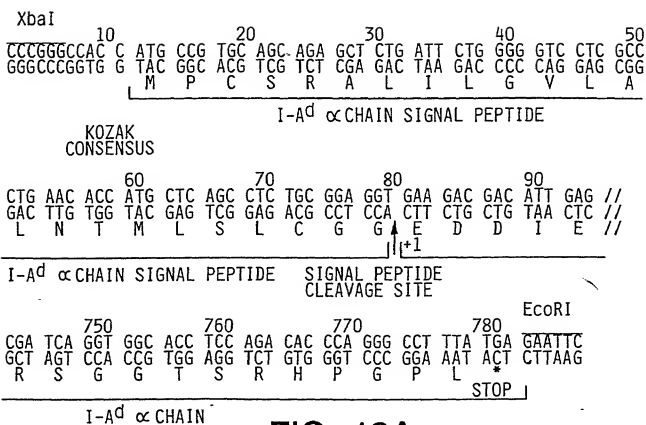


FIG. 18A

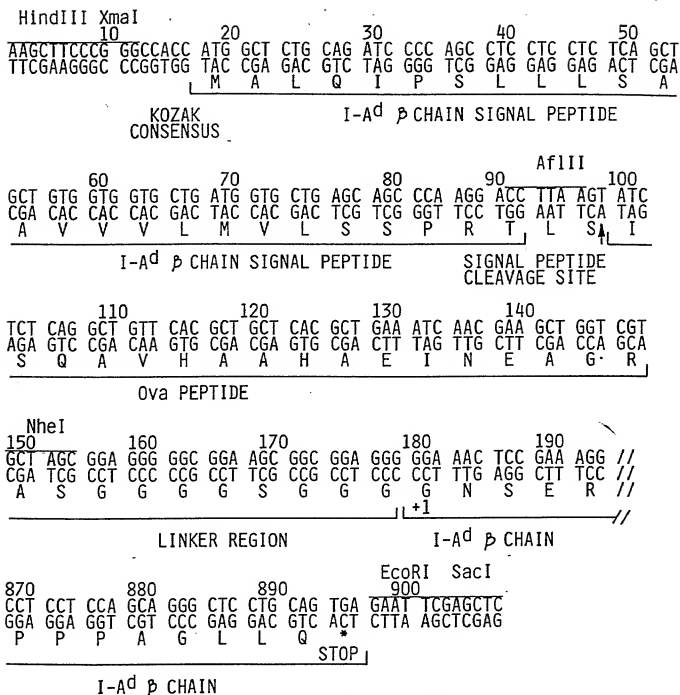


FIG. 18B

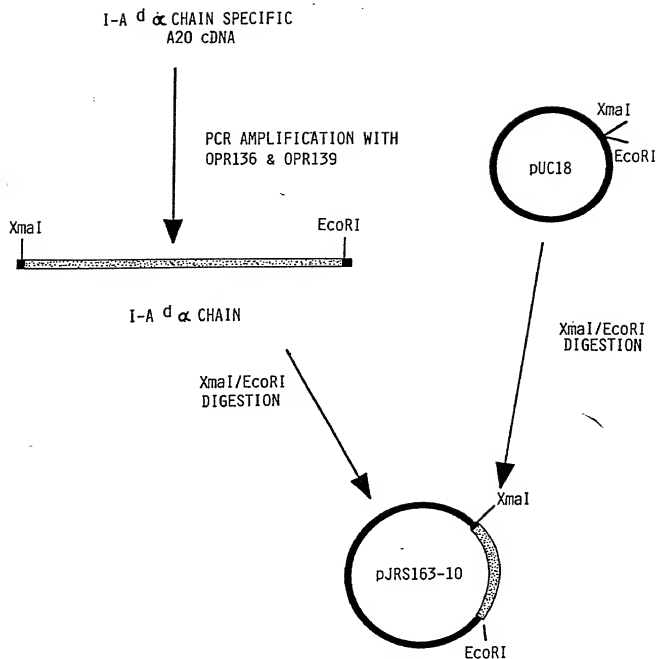


FIG. 19A

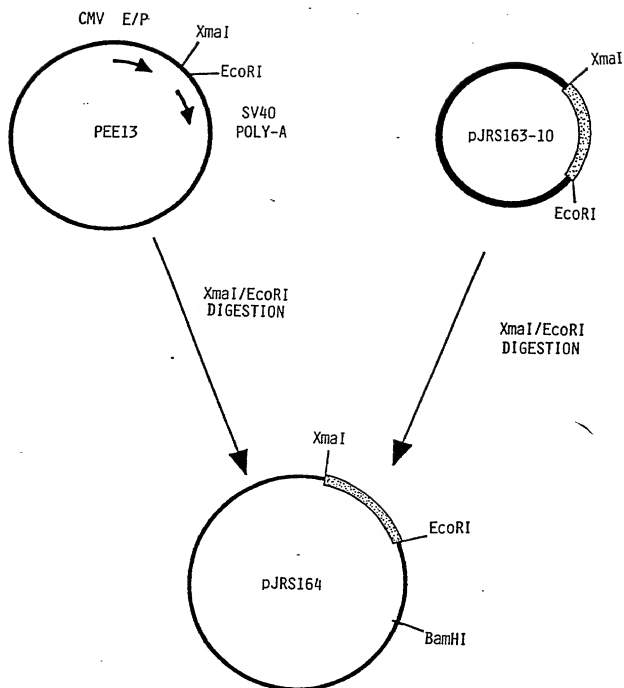


FIG. 19B

09848164-050301

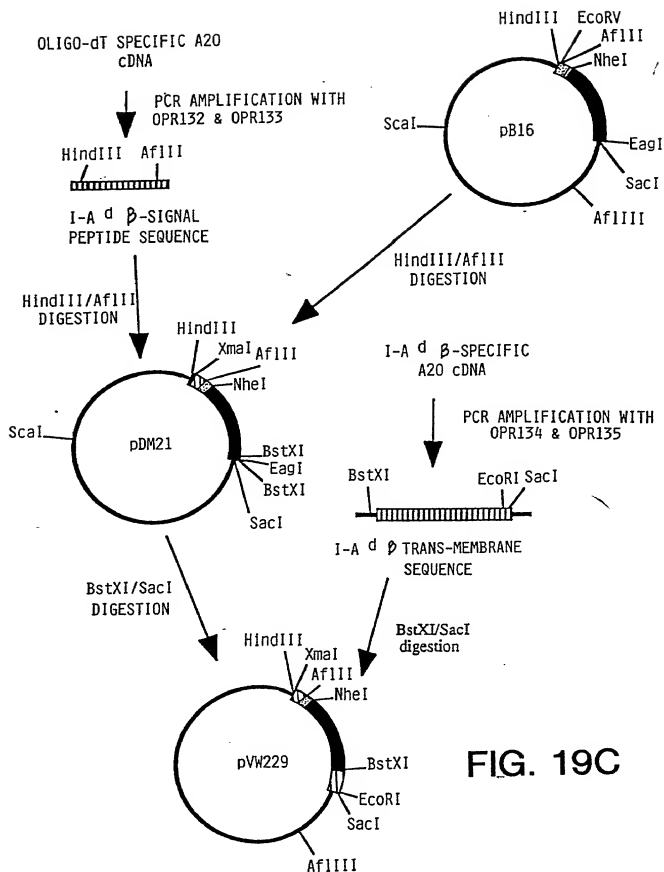


FIG. 19C



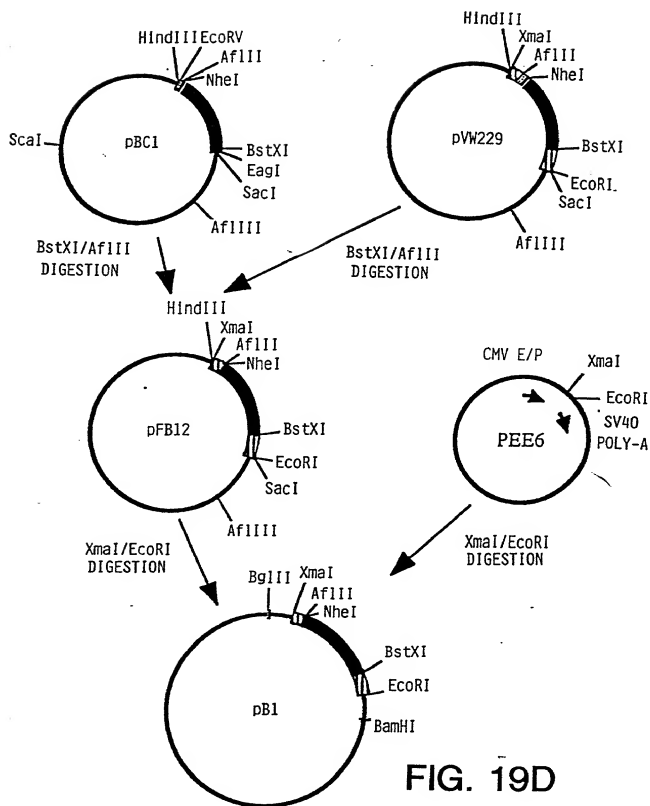


FIG. 19D

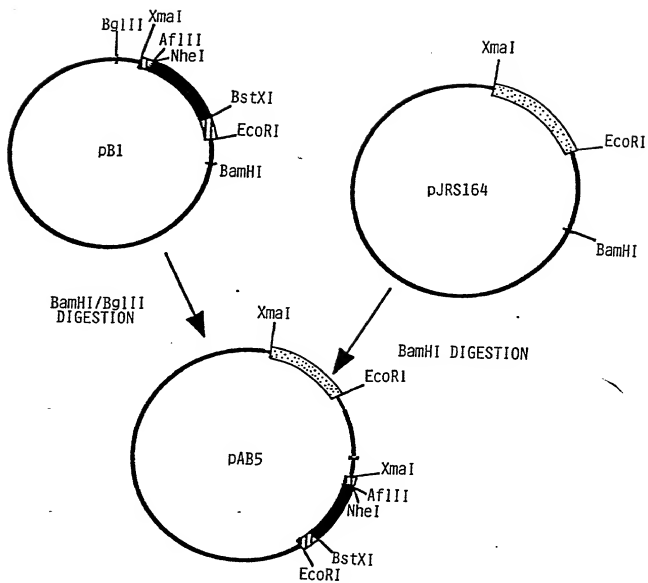


FIG. 19E

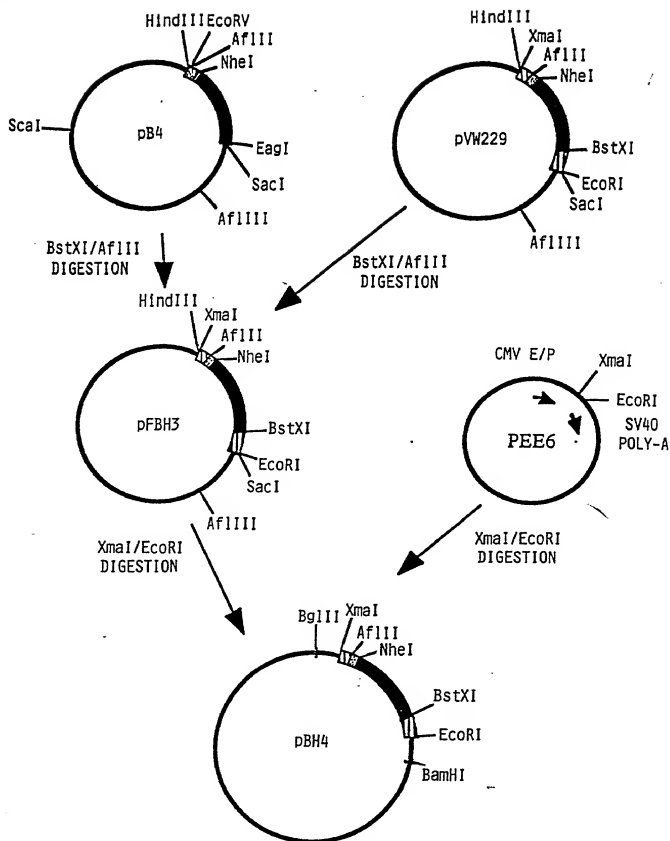


FIG. 19F

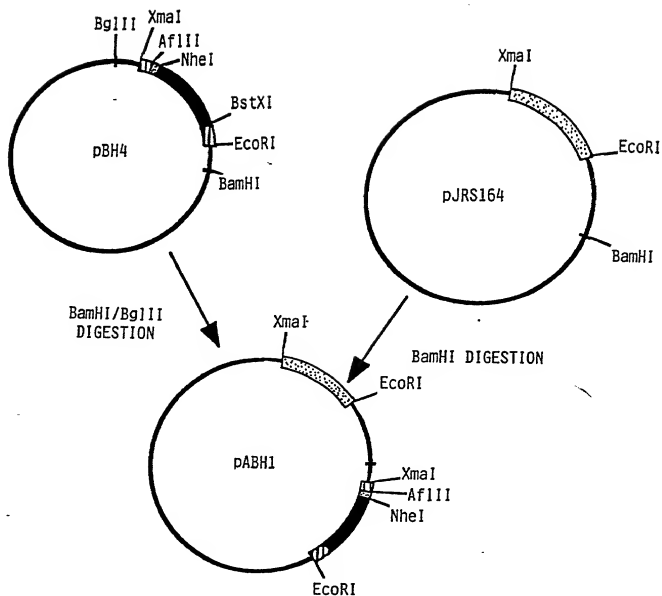


FIG. 19G

5' -CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA  
GC-3'

I-A<sup>d</sup>  $\beta$  signal peptide back primer with Kozak consensus for CellTech vector - AflII site  
5'-CCC CCC ACT TAA GGT CCT TGG·GCT GCT CAG CAC C-3'

I-A<sup>d</sup>  $\beta$  transmembrane front primer for CellTech vector - BstXI sites  
5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

I-A<sup>d</sup>  $\beta$  transmembrane back primer for CellTech vector - SstI, EcoRI sites  
5'-CCC CCC GAG CTC GAA TCC TCA CTG CAG GAG CCC TGC TGG-3'

I-A<sup>d</sup>  $\alpha$  signal peptide front primer with Kozak consensus for CellTech vector - HindIII/XmaI sites  
5'-CCC CCC AAG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC  
TG-3'

I-A<sup>d</sup>  $\alpha$  transmembrane primer for CellTech vector - SstI/EcoRI sites  
5'-CCC CCC GAG CTC GAA TCC TCA TAA AGG CCC TGG GTG TCT G-3'

Murine B7-1 front primer with Kozak consensus for CloneTech vector - NotI site  
5'-CCC CCC CCG CGG CCG CCC CAC CAT GGG ACT GAG TAA CAT TCT  
C-3'

Murine B7-1 BACK primer for CloneTech vector - NotI site  
5'-CCC CCC GCG GCC GCT TTA AAA ACA TGT ATC ACT TTT-3'

FIG. 20

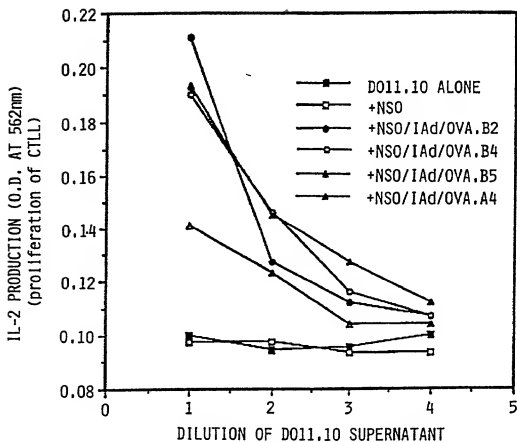


FIG. 21

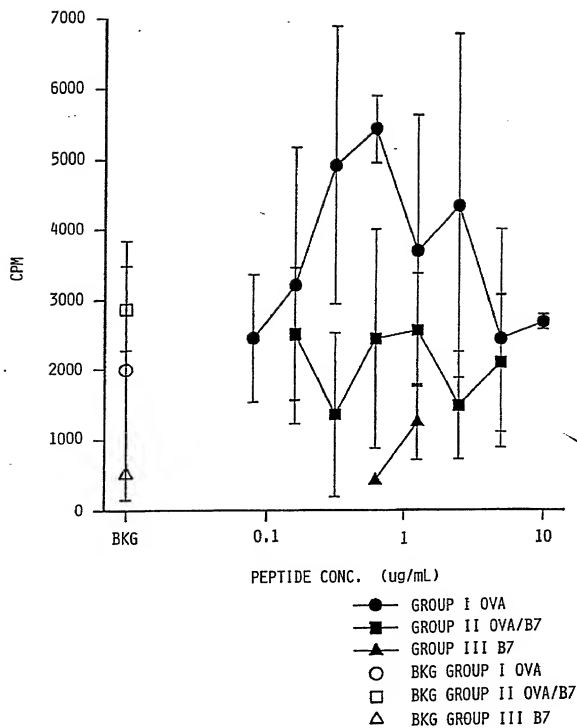


FIG. 22

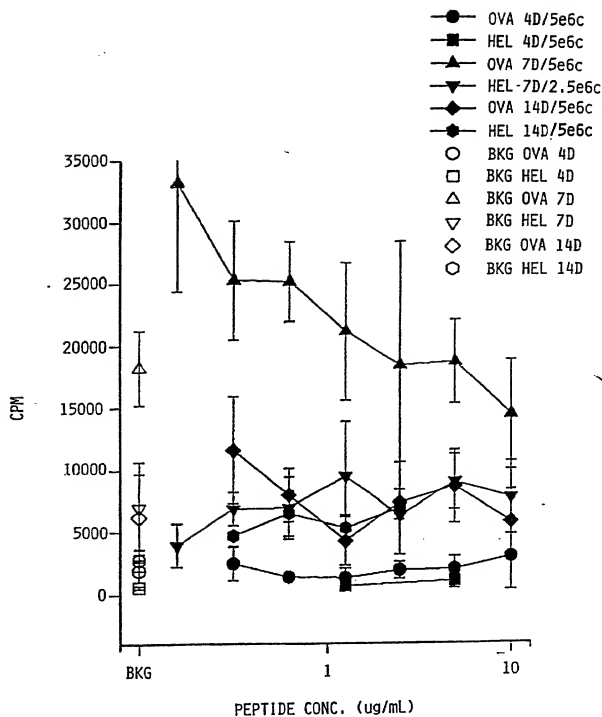


FIG. 23



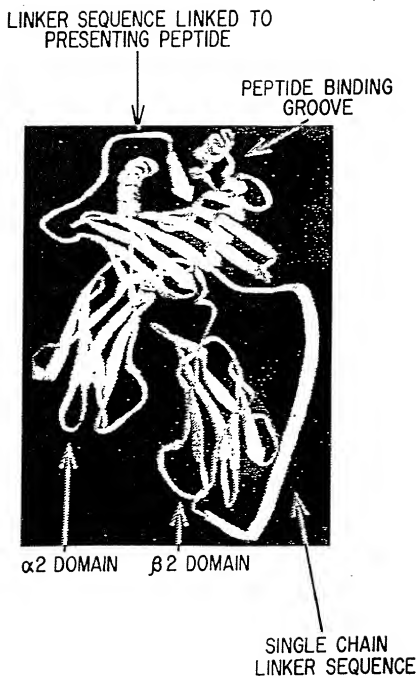


FIG.24

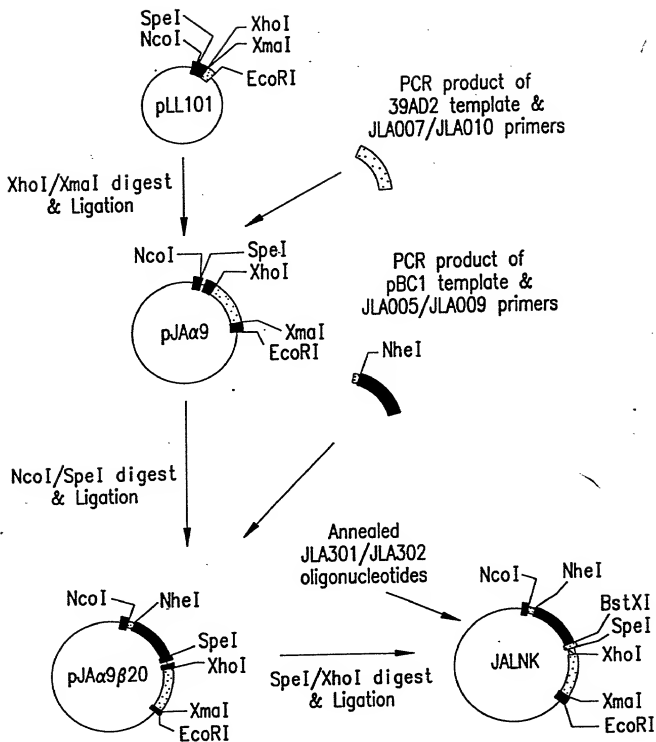


FIG.25A

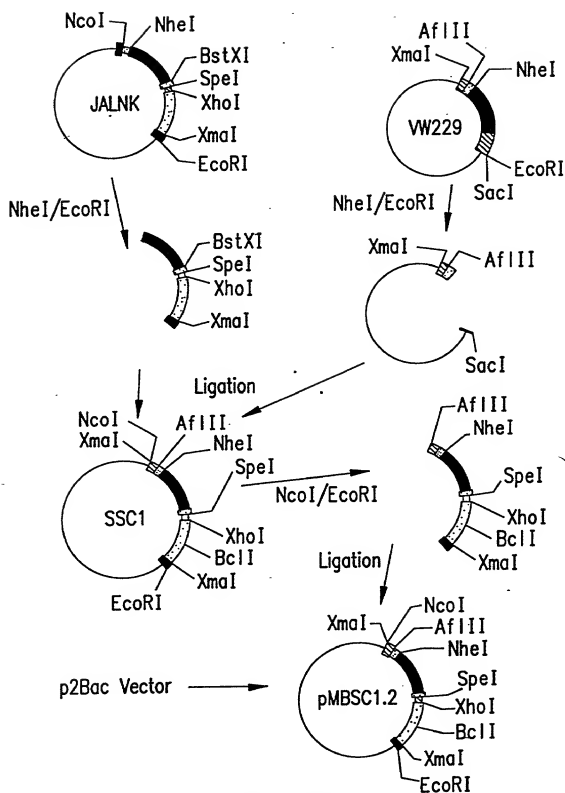


FIG.25B

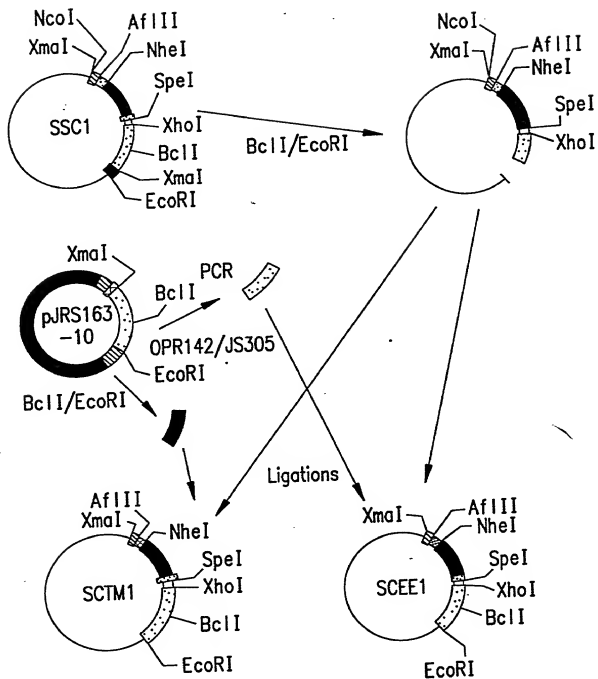


FIG.25C

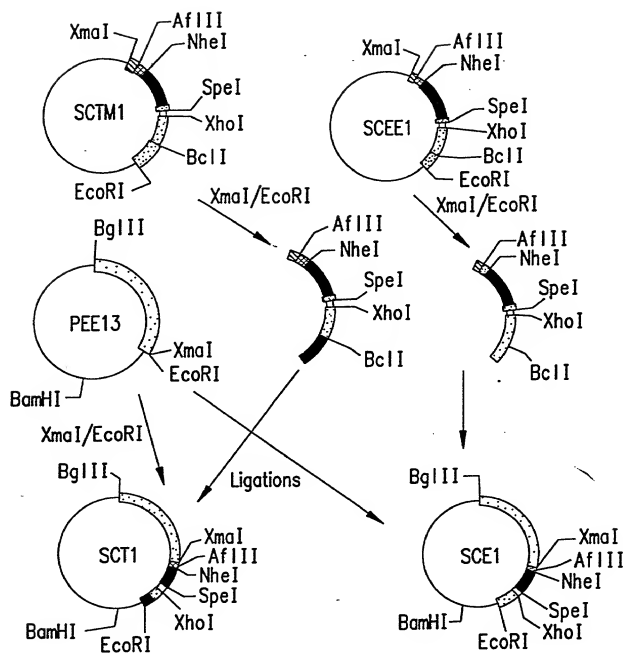


FIG.25D

JLA-005

5' - CCCCCGCCATGGCCGCTAGCGGAGGGGGCGGAAGC - 3'

JLA-007

5' - CCCGGGGCCTCGAGTGAAGACGACATTGAGGCCGAC - 3'

JLA-009

5' - CCCCCCACTAGTCCACTCCACAGTGATGGGGCT - 3'

JLA-010

5' - CCCCCCCCCGGGACCAGTGTTCAGAACCGGCTCCTC - 3'

JLA-301

5' - TCGAGGAACCGCCACCGCCAGAACCGCCGCCACCGGA-  
ACCACCAACCGCGCTGCCACCGCCACCA - 3'

JLA-302

5' - CTAGTGGTGGCGGTGGCAGCGCGGTGGTGGTTCCGG-  
TGGCGGCGGTTCTGGCGGTGGCGGTTCC - 3'

OPR-142

5' - CTTGGGAATCTTGACTAAGAGG - 3'

JS-305

5' - CAGGTCAATTCTCATTCATCGGCATGTA CTCTCTT-  
CCTCCAGTGTTTCAGAACCGG - 3'

FIG.26

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10 20 30 40 50  
 \* \* \* \* \*  
 CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC TCA GCT GCT GTG GTG  
 GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC  
 M A L Q I P S L L L S A A V V>

<----- I-Ad  $\beta$ -CHAIN LEADER ----->

60 70 80 90  
 \* \* \* \* \*  
 GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT  
 CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA  
 V L M V L S S P R T L S I S Q A>

100 110 120 130 140  
 \* \* \* \* \*  
 GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA  
 CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT  
 V H A A H A E I N E A G R A S G>  
 ----- OVA 323-339 ----->

150 160 170 180 190  
 \* \* \* \* \*  
 GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC  
 CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG  
 G G G S G G G G N S E R H F V V>

-- 10 AMINO ACID LINKER-->----- I-Ad  $\beta$ -1 DOMAIN ----->

200 210 220 230 240  
 \* \* \* \* \*  
 CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG  
 GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC  
 Q F K G E C Y Y T N G T Q R I R>

250 260 270 280 290  
 \* \* \* \* \*  
 CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC  
 GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG  
 L V T R Y I Y N R E E Y V R Y D>

FIG.27A

09848167-050301

300 310 320 330  
 \* \* \* \*  
 AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC  
 TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG  
 S D V G E Y R A V T E L G R P D>

340 350 360 370 380  
 \* \* \* \* \*  
 GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC  
 CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG  
 A E Y W N S Q P E I L E R T R A>

390 400 410 420 430  
 \* \* \* \* \*  
 GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC  
 CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG  
 E V D T A C R H N Y E G P E T S>

440 450 460 470 480  
 \* \* \* \* \*  
 ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC  
 TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG  
 T S L R R L E Q P N V A I S L S>  
 --- I-Ad  $\beta$ -1 DOMAIN --<----- I-Ad  $\beta$ -2 DOMAIN -----

490 500 510 520 530  
 \* \* \* \* \*  
 AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA  
 TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT  
 R T E A L N H H N T L V C S V T>

540 550 560 570  
 \* \* \* \*  
 GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG  
 CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC  
 D F Y P A K I K V R W F R N G Q>

FIG. 27B



580                      590                      600                      610                      620  
 \*                      \*                      \*                      \*                      \*  
 GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC  
 CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG  
 E E T V G V S S T Q L I R N G D>

630                      640                      650                      660                      670  
 \*                      \*                      \*                      \*                      \*  
 TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA  
 ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT  
 W T F Q V L V M L E M T P H Q G>

680                      690                      700                      710                      720  
 \*                      \*                      \*                      \*                      \*  
 GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC  
 CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTT TCG GGG TAG  
 E V Y T C H V E H P S L K S P I>  
 ----- I-Ad  $\beta$ -2 DOMAIN -----

730                      740                      750                      760                      770  
 \*                      \*                      \*                      \*                      \*  
 ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC  
 TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG  
 T V E W T S G G G G S G G G G S>  
 -----><----- 24 AMINO ACID LINKER -----

780                      790                      800                      810  
 \*                      \*                      \*                      \*  
 GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT  
 CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA  
 G G G G S G G G G S S S E D D I>  
 -----><-----

820                      830                      840                      850                      860  
 \*                      \*                      \*                      \*                      \*  
 GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT  
 CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA  
 E A D H V G F Y G T T V Y Q S P>  
 ----- I-Ad  $\alpha$ -1 DOMAIN -----

FIG.27C

```

      870          880          890          900          910
      *           *           *           *           *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
G   D   I   G   Q   Y   T   H   E   F   D   G   D   E   L   F>
-----

      920          930          940          950          960
      *           *           *           *           *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
Y   V   D   L   D   K   K   K   T   V   W   R   L   P   E   F>
-----

      970          980          990          1000         1010
      *           *           *           *           *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
G   Q   L   I   L   F   E   P   Q   G   G   L   Q   N   I   A>
-----

      1020         1030         1040         1050
      *           *           *           *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
A   E   K   H   N   L   G   I   L   T   K   R   S   N   F   T>
-----
                                I-Ad  $\alpha$ -1 DOMAIN
-----

1060          1070          1080          1090          1100
  *           *           *           *           *
CCA GCT ACC AAT GAG GCT CCT CCA CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
P   A   T   N   E   A   P   Q   A   T   V   F   P   K   S   P>
-----
                                I-Ad  $\alpha$ -2 DOMAIN
-----

1110          1120          1130          1140          1150
  *           *           *           *           *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
V   L   L   G   Q   P   N   T   L   I   C   F   V   D   N   I>
-----

```

FIG.27D

1160                      1170                      1180                      1190                      1200  
 \*                      \*                      \*                      \*                      \*  
 TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC  
 AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG  
 F P P V I N I T W L R N S K S V>

-----

1210                      1220                      1230                      1240                      1250  
 \*                      \*                      \*                      \*                      \*  
 ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC  
 TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG  
 T D G V Y E T S F L V N R D H S>

-----

1260                      1270                      1280                      1290  
 \*                      \*                      \*                      \*  
 TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT  
 AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA  
 F H K L S Y L T F I P S D D D I>

-----

1300                      1310                      1320                      1330                      1340  
 \*                      \*                      \*                      \*                      \*  
 TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA  
 ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT  
 Y D C K V E H W G L E E P V L K>

----- I-Ad  $\alpha$ -2 DOMAIN -----

1350                      1360                      1370                      1380  
 \*                      \*                      \*                      \*  
 CAC TGG TCC CGG GCT AGT CAC CAT CAC CAT CAT CAC TAG  
 GTG ACC AGG GCC CGA TCA GTG GTA GTG GTA GTG ATC  
 H W S R A S H H H H H H \*>

----->X----- 6 X HIS tag ----->

FIG.27E

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```

      10      20      30      40      50
      *      *      *      *      *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M A L G I P S L L L S A A V V>
<----- I-Ad β CHAIN LEADER ----->

      60      70      80      90
      *      *      *      *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
V L M V L S S P R T L S I S Q A>
-----><-----

100      110      120      130      140
  *      *      *      *      *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CAG TCG CCT
V H A A H A E I N E A G R A S G>
----- OVA 323-339 -----><-----

150      160      170      180      190
  *      *      *      *      *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
G G G S G G G N S E R H F V V>
-- 10 AMINO ACID LINKER --><----- I-Ad β-1 DOMAIN ----->

200      210      220      230      240
  *      *      *      *      *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TCC TTG CCC TGC GTC GCG TAT GCC
Q F K G E C Y Y T N G T Q R I R>
-----><-----

250      260      270      280      290
  *      *      *      *      *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC ATG CAC GCG ATG CTG
L V T R Y I Y N R E E Y V R Y D>
-----><-----

```

FIG.28A

09648164-050301

```

      300      310      320      330
      *      *      *      *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG GCG CAC TGG CTC GAC CCC GCC GGT CTG
S D V G E Y R A V T E L G R P D>
-----

340      350      360      370      380
*      *      *      *      *
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
A E Y W N S Q P E I L E R T R A>
-----

390      400      410      420      430
*      *      *      *      *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC GCG ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
E V D T A C R H N Y E G P E T S>
-----

440      450      460      470      480
*      *      *      *      *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
T S L R R L E Q P N V A I S L S>
--- I-Ad  $\beta$ -1 DOMAIN --><----- I-Ad  $\beta$ -2 DOMAIN -----

490      500      510      520      530
*      *      *      *      *
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
R T E A L N H H N T L V C S V T>
-----

540      550      560      570
*      *      *      *
GAT TTC TAC CCA GCC AAG ATC AAA GTG GCG TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
D F Y P A K I K V R W F R N G Q>
-----

```

FIG.28B

580                      590                      600                      610                      620  
 \*                      \*                      \*                      \*                      \*  
 GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC  
 CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG  
 E E T V G V S S T Q L I R N G D>

630                      640                      650                      660                      670  
 \*                      \*                      \*                      \*                      \*  
 TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA  
 ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT  
 W T F Q V L V M L E M T P H Q G>

680                      690                      700                      710                      720  
 \*                      \*                      \*                      \*                      \*  
 GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC  
 CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG  
 E V Y T C H V E H P S L K S P I>  
 ----- I-Ad  $\beta$ -2 DOMAIN -----

730                      740                      750                      760                      770  
 \*                      \*                      \*                      \*                      \*  
 ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC  
 TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG  
 T V E W T S G G G G S G G G G S>  
 -----><----- 24 AMINO ACID LINKER -----

780                      790                      800                      810  
 \*                      \*                      \*                      \*  
 GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT  
 CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA  
 G G G G S G G G G S S S E D D I>  
 -----><-----

820                      830                      840                      850                      860  
 \*                      \*                      \*                      \*                      \*  
 GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT  
 CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA  
 E A D H V G F Y G T T V Y Q S P>  
 ----- I-Ad  $\alpha$ -1 DOMAIN -----

FIG.28C

870                      880                      890                      900                      910  
 \*                      \*                      \*                      \*                      \*  
 GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC  
 CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG  
 G D I G. Q Y T H E F D G D E L F>

920                      930                      940                      950                      960  
 \*                      \*                      \*                      \*                      \*  
 TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT  
 ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA  
 Y V D L D K K K T V W R L P E F>

970                      980                      990                      1000                      1010  
 \*                      \*                      \*                      \*                      \*  
 GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT  
 CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA  
 G Q L I L F E P Q G G L Q N I A>

1020                      1030                      1040                      1050  
 \*                      \*                      \*                      \*  
 GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC  
 CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG  
 A E K H N L G I L T K R S N F T>  
 ----- I-Ad  $\alpha$ -1 DOMAIN -----

1060                      1070                      1080                      1090                      1100  
 \*                      \*                      \*                      \*                      \*  
 CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT  
 GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA  
 P A T N E A P Q A T V F P K S P>  
 -----><----- I-Ad  $\alpha$ -2 DOMAIN -----

1110                      1120                      1130                      1140                      1150  
 \*                      \*                      \*                      \*                      \*  
 GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC  
 CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG  
 V L L G Q P N T L I C F V D N I>

FIG.28D

008463164-050301

```

      1160      1170      1180      1190      1200
      *        *        *        *        *
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
F   P   P   V   I   N   I   T   W   L   R   N   S   K   S   V>
-----

      1210      1220      1230      1240      1250
      *        *        *        *        *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
T   D   G   V   Y   E   T   S   F   L   V   N   R   D   H   S>
-----

      1260      1270      1280      1290
      *        *        *        *
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
F   H   K   L   S   Y   L   T   F   I   P   S   D   D   D   I>
-----

1300      1310      1320      1330      1340
*        *        *        *        *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTY
Y   D   C   K   V   E   H   W   G   L   E   E   P   V   L   K>
----- I-Ad  $\alpha$ -2 DOMAIN -----

      1350      1360      1370      1380      1390
      *        *        *        *        *
CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT
GTG ACC CTT GGA CTC TAA GGT CGG GGG TAC AGT CTC GAC TGT CTT TGA
H   W   E   P   E   I   P   A   P   M   S   E   L   T   E   T>
-----><----- I-Ad  $\alpha$ -TM DOMAIN -----

      1400      1410      1420      1430      1440
      *        *        *        *        *
GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG
CAC CAC ACA CGG GAC CCC AAC AGA CAC CCG GAA CAC CCG TAG CAC CAC
V   V   C   A   L   G   L   S   V   G   L   V   G   I   V   V>
-----

```

FIG.28E



	1450		1460		1470		1480		1490						
	*		*		*		*		*						
GGC	ACC	ATC	TTC	ATC	ATT	CAA	GGC	CTG	CGA	TCA	GGT	GGC	ACC	TCC	AGA
CCG	TGG	TAG	AAG	TAG	TAA	GTT	CCG	GAC	GCT	AGT	CCA	CCG	TGG	AGG	TCT
G	T	I	F	I	I	Q	G	L	R	S	G	G	T	S	R>

---

CAC CCA GGG CCT TTA TGA  
 GTG GGT CCC GGA AAT ACT  
 H P G P L \*>  
 - I-Ad  $\alpha$ -TM DOMAIN ->

FIG.28F

```

      10      20      30      40      50
      *      *      *      *      *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M   A   L   Q   I   P   S   L   L   L   S   A   A   V   V>
<----- I-Ad  $\beta$  CHAIN LEADER ----->

      60      70      80      90
      *      *      *      *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
      V   L   M   V   L   S   S   P   R   T   L   S   I   S   Q   A>
----->-----<-----

100      110      120      130      140
  *      *      *      *      *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
      V   H   A   A   H   A   E   I   N   E   A   G   R   A   S   G>
----- OVA 323-339 -----><-----

      150      160      170      180      190
      *      *      *      *      *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
      G   G   G   S   G   G   G   G   N   S   E   R   H   F   V   V>
-- 10 AMINO ACID LINKER --><----- I-Ad  $\beta$ -1 DOMAIN -----<-----

      200      210      220      230      240
      *      *      *      *      *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
      Q   F   K   G   E   C   Y   Y   T   N   G   T   Q   R   I   R>
----->-----<-----

      250      260      270      280      290
      *      *      *      *      *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
      L   V   T   R   Y   I   Y   N   R   E   E   Y   V   R   Y   D>
----->-----<-----

```

FIG.29A

```

      300      310      320      330
      *        *        *        *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
S   D   V   G   E   Y   R   A   V   T   E   L   G   R   P   D>
-----

340      350      360      370      380
*        *        *        *        *
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
A   E   Y   W   N   S   Q   P   E   I   L   E   R   T   R   A>
-----

390      400      410      420      430
*        *        *        *        *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
E   V   D   T   A   C   R   H   N   Y   E   G   P   E   T   S>
-----

440      450      460      470      480
*        *        *        *        *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
T   S   L   R   R   L   E   Q   P   N   V   A   I   S   L   S>
--- I-Ad  $\beta$ -1 DOMAIN -><----- I-Ad  $\beta$ -2 DOMAIN -----

490      500      510      520      530
*        *        *        *        *
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
R   T   E   A   L   N   H   H   N   T   L   V   C   S   V   T>
-----

540      550      560      570
*        *        *        *
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
D   F   Y   P   A   K   I   K   V   R   W   F   R   N   G   Q>
-----

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FIG.29B

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```

580          590          600          610          620
*          *          *          *          *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
E   E   T   V   G   V   S   S   T   Q   L   I   R   N   G   D>
-----

        630          640          650          660          670
        *          *          *          *          *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
W   T   F   Q   V   L   V   M   L   E   M   T   P   H   Q   G>
-----

        680          690          700          710          720
        *          *          *          *          *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
E   V   Y   T   C   H   V   E   H   P   S   L   K   S   P   I>
-----
                                I-Ad β-2 DOMAIN -----

        730          740          750          760          770
        *          *          *          *          *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
T   V   E   W   T   S   G   G   G   G   S   G   G   G   G   S>
-----
                                24 AMINO ACID LINKER -----

        780          790          800          810
        *          *          *          *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
G   G   G   G   S   G   G   G   G   S   S   S   E   D   D   I>
-----

        820          830          840          850          860
        *          *          *          *          *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
E   A   D   H   V   G   F   Y   G   T   T   V   Y   Q   S   P>
-----
                                I-Ad α-1 DOMAIN -----

```

FIG.29C

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```

      870          880          890          900          910
      *           *           *           *           *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
G   D   I   G   Q   Y   T   H   E   F   D   G   D   E   L   F>
-----

      920          930          940          950          960
      *           *           *           *           *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
Y   V   D   L   D   K   K   K   T   V   W   R   -L   P   E   F>
-----

      970          980          990          1000         1010
      *           *           *           *           *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA GCT GAC GTT TTG TAT CGA
G   Q   L   I   L   F   E   P   Q   G   G   L   Q   N   I   A>
-----

      1020         1030         1040         1050
      *           *           *           *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
A   E   K   H   N   L   G   I   L   T   K   R   S   N   F   T>
----- I-Ad α-1 DOMAIN -----

1060          1070          1080          1090          1100
*            *            *            *            *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
P   A   T   N   E   A   P   Q   A   T   V   F   P   K   S   P>
-----><----- I-Ad α-2 DOMAIN -----

1110          1120          1130          1140          1150
*            *            *            *            *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
V   L   L   G   Q   P   N   T   L   I   C   F   V   D   N   I>
-----

```

FIG.29D

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```

      1160      1170      1180      1190      1200
      *        *        *        *        *
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
F   P   P   V   I   N   I   T   W   L   R   N   S   K   S   V>
-----

      1210      1220      1230      1240      1250
      *        *        *        *        *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
T   D   G   V   Y   E   T   S   F   L   V   N   R   D   H   -S>
-----

      1260      1270      1280      1290
      *        *        *        *
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
F   H   K   L   S   Y   L   T   F   I   P   S   D   D   D   I>
-----

1300      1310      1320      1330      1340
*        *        *        *        *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
Y   D   C   K   V   E   H   W   G   L   E   E   P   V   L   K>
-----
I-Ad α-2 DOMAIN -----

      1350      1360      1370      1380
      *        *        *        *
CAC TGG GAG GAA GAA GAG TAC ATG CCG ATG GAA TGA
GTG ACC CTC CTT CTT CTC ATG TAC GGC TAC CTT ACT

H   W   E   E   E   E   Y   M   P   M   E   >
-----><----- EE TAG ----->

```

FIG.29E

00848164-050204

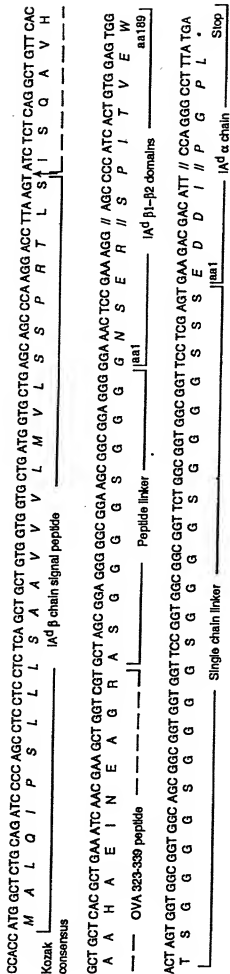


FIG.30

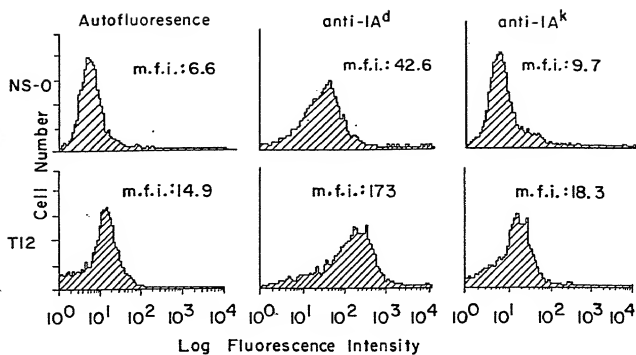


FIG. 3IA

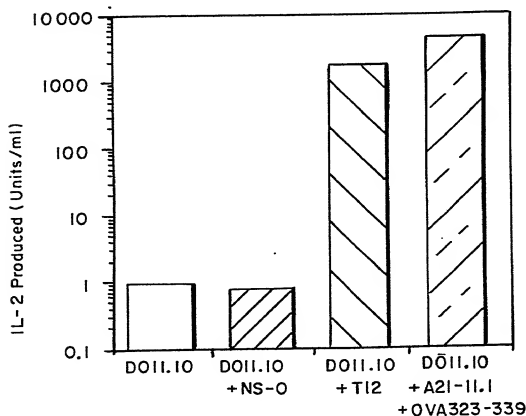


FIG. 3IB



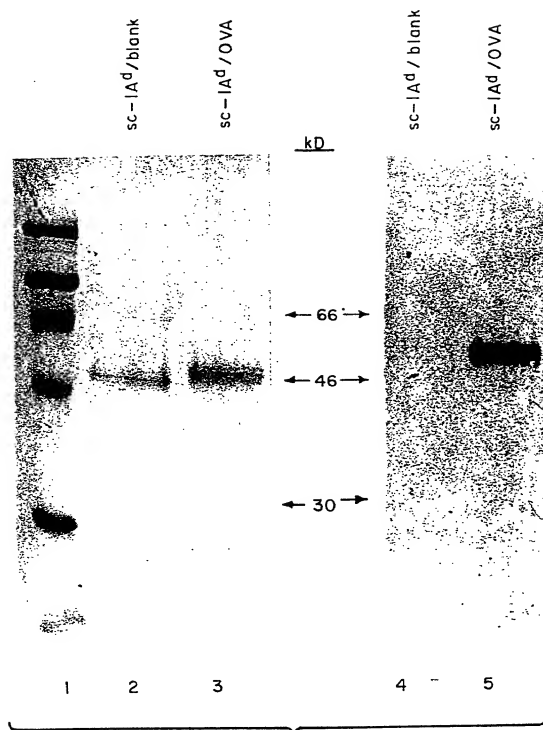


FIG.32

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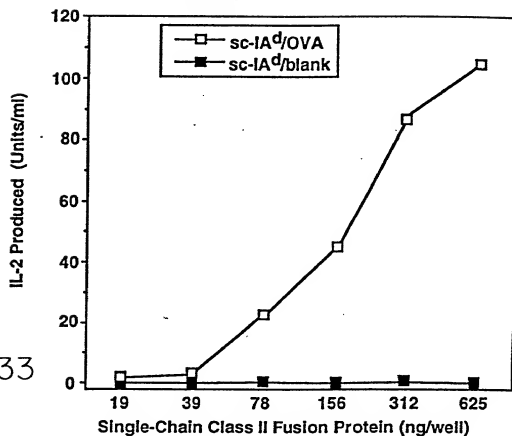


FIG.33

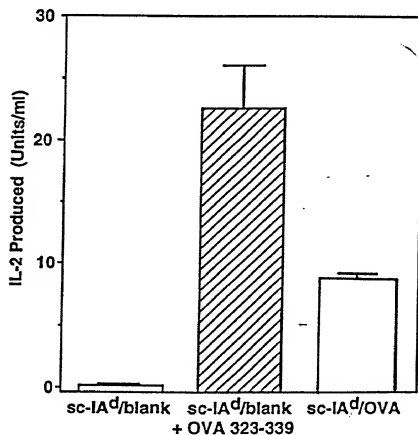


FIG.34C

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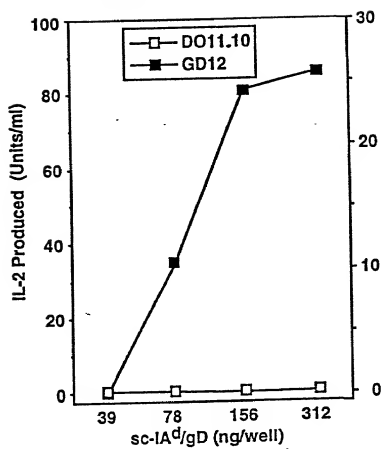


FIG.34A

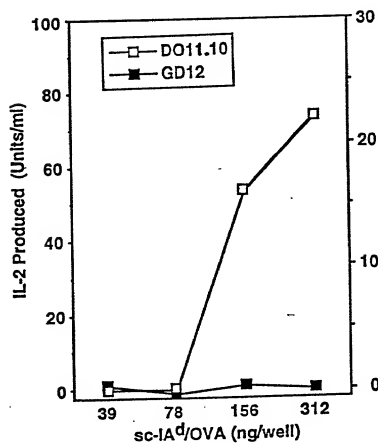


FIG.34B

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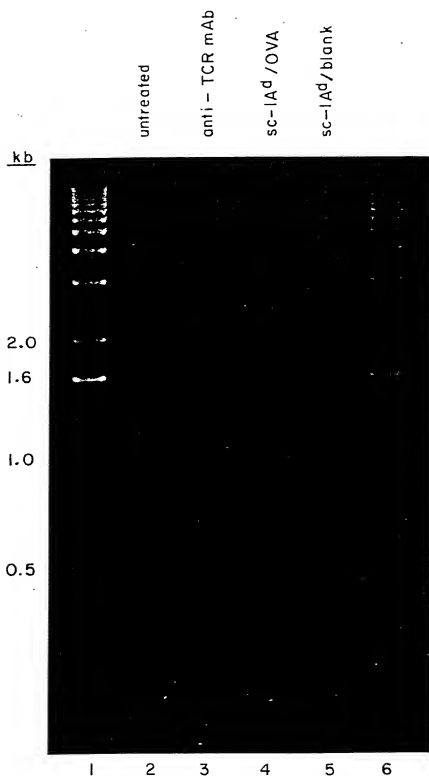


FIG. 35

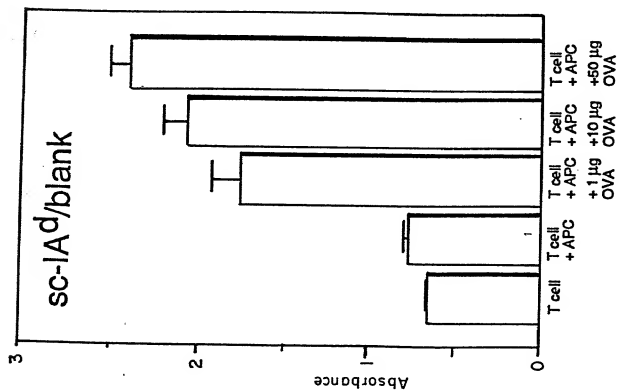


FIG. 36A

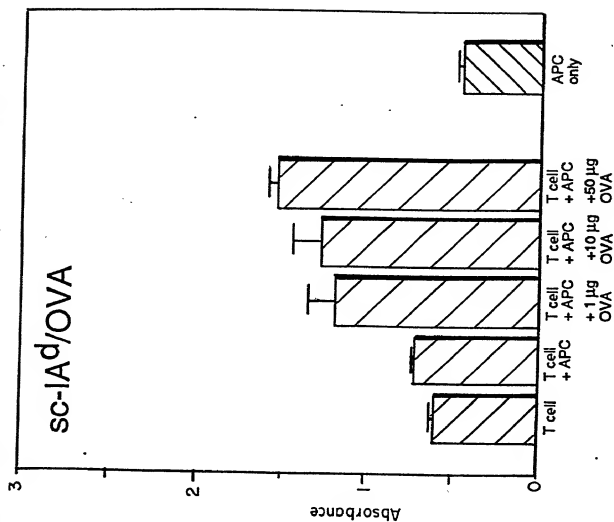


FIG. 36B